GENOTYPIC AND PHENOTYPIC ANTIMICROBIAL RESISTANCE PROFILES OF STAPHYLOCOCCUS HAEMOLYTICUS AND S. EPIDERMIDIS FROM GERMAN DAIRY FARMS WITH A HISTORY OF MRSA-DETECTION.

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INTRODUCTION

Staphylococci are frequently found in different niches on dairy farms. Beside the best known and investigated species, Staphylococcus (S.) aureus, and non-aureus staphylococci (NAS), inhabit animals and the farm environment. Regarding virulence and human health, the species S. epidermidis and S. haemolyticus were reported to cause severe infections in hospitals worldwide. Since staphylococci may express resistance to a varying number of antibiotics, the treatment of staphylococcal infections can be complicated. The aim of the study was to evaluate the antimicrobial resistance (AMR) potential of S. haemolyticus and S. epidermidis from German dairy farms.

METHODOLOGY

During a sampling campaign carried out from September 2018 to December 2019 on pre-selected German dairy farms with a history of MRSA-detection, various staphylococcal isolates were retrieved from bulk tank milk, quarter milk samples and swab samples from calves and heifers as well as from the environment, such as from teat cups or dust samples, using selective isolation procedures primarily to detect MRSA. Beside other species, S. haemolyticus and S. epidermidis were found in different niches of the dairy farms. For an evaluation of the AMR potential of these species, whole-genome sequencing and antimicrobial susceptibility testing were carried out for a selection of seven S. haemolyticus and 14 S. epidermidis isolates. AMR genes were predicted according to an in-house bioinformatics pipeline using NCBI AMRfinder, and phenotypic AMR against 19 antibiotics was evaluated according to EUCAST ECOFFs.

RESULTS

The S. haemolyticus isolates were characterised by sequence types (ST) 3, 8 and 30 and SCCmec type V elements. The AMR gene count ranged from 8 to 16 genes with a prediction of resistance to up to eight different antimicrobial classes. Accordingly, phenotypic resistance to chloramphenicol (1/7), ciprofloxacin (6/7), clindamycin (2/7), gentamicin (5/7), erythromycin (7/7), cefoxitin (7/7), fusidic acid (2/7), kanamycin (6/7), penicillin (7/7), streptomycin (3/7), sulfamethoxazole (6/7), quinupristin-dalfopristin (1/7), tetracycline (7/7) and trimethoprim (6/7) was determined.

The S. epidermidis isolates were characterised by STs 10, 59, 89 and 100 and SCCmec type IVa and V elements. The AMR gene count ranged from 6 to 16 genes with a prediction of resistance to up to eight different antimicrobial classes. Accordingly, phenotypic resistance to chloramphenicol (7/14), ciprofloxacin (1/14), gentamicin (2/14), erythromycin (1/14), cefoxitin (13/14), fusidic acid (3/14), kanamycin (4/14), penicillin (12/14), streptomycin (8/14), sulfamethoxazole (1/14), tetracycline (6/14) and trimethoprim (3/14) was determined.

DISCUSSION

When interpreting the results, it is important to consider that the bacteria were isolated using the selective isolation of resistant bacteria from farms with a history of MRSA detection. On these pre-selected farms, multidrug-resistant S. haemolyticus and S. epidermidis were found in different niches. The detection of two different S. epidermidis sequence types on the same farm shows a spread of different lineages across the farm environment. Thirteen isolates harboured at least 10 AMR genes. Accordingly, phenotypic AMR to several classes of antibiotic was detected. S. haemolyticus isolates were resistant to a higher number of antibiotics than the investigated S. epidermidis isolates, exhibiting resistances to up to 13 of the 19 tested antibiotics. Since S. haemolyticus and S. epidermidis were occasionally found in hospitals and may express different virulence factors, multidrug-resistance in these species might lead to difficult-to-treat infections. Moreover, these NAS species might serve as an AMR gene reservoir for potentially pathogenic staphylococcal species such as S. aureus. Therefore, it is highly important to monitor the AMR repertoire of staphylococci on animal farms.